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GAATTCCTGCAGCTCAGCAGCCGCCAGAGCAGGACGAACCGCCAATCGCAAGGCACC  
1 -----+-----+-----+-----+-----+-----+ 60  
CTTAAGGACGTCGAGTCGTTCGGCGGCGGTCTCGTCCTGCTTGGCGGTTAGCGTTCCTGG

TCTGAGAACTTCAGGATGCAGATGTCTCCAGCCCTCACCTGCCTAGTCCTGGGCCTGGCC  
61 -----+-----+-----+-----+-----+-----+ 120  
AGACTCTTGAAAGTCCTACGTCTACAGAGGTTCGGGAGTGGACGGATCAGGACCCGGACCGG

aa M Q M S P A L T C L V L G L A -  
| Signal Peptide  
CTGTCTTTGGTGAAGGGTCTGCTGTGCACCATCCCCCATCTACGTGGCCACCTGGCC  
121 -----+-----+-----+-----+-----+-----+ 180  
GAACAGAAACCACCTCCAGACGACCGTGGTAGGGGGTAGGATGCACCGGGTGGACCGG

aa L V F G E G S A | V H H P P S Y V A H L A 12  
Start Mature Protein  
TCAGACTTCGGGGTGAGGGTGTTCAGCAGGTGGCGCAGGCCTCCAAGGACCGCAACGTG  
181 -----+-----+-----+-----+-----+-----+ 240  
AGTCTGAAGCCCCACTCCACAAAGTCGTCCACCGCGTCCGGAGGTTCTGGCGTTGCAC

aa S D F G V R V F Q Q V A Q A S K D R N V 32  
GTTTCTCACCCTATGGGGTGGCCTCGGTGTTGGCCATGCTCCAGCTGACAACAGGAGGA  
241 -----+-----+-----+-----+-----+-----+ 300  
CAAAAGAGTGGGATACCCACCGGAGCCCAACCGGTACGAGGTGACTGTTGTCTCTCT

aa V F S P Y G V A S V L A M L Q L T T G G 52  
GAAACCCAGCAGCAGATTCAAGCAGCTATGGGATTCAAGATTGATGACAAGGGCATGGCC  
301 -----+-----+-----+-----+-----+-----+ 360  
CTTTGGGTCGTCTAGTTCGTTCGATACCCCTAAGTTCTAACTACTGTTCCCGTACCGG

aa E T Q Q Q I Q A A M G F K I D D K G M A 72  
CCCCCCTCCGGCATCTGTACAAGGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGC  
361 -----+-----+-----+-----+-----+-----+ 420  
GGGCGGGAGGCCGTAGACATGTTCTCGAGTACCCCGGTACCTTGTTCTACTCTAGTCG

aa P A L R H L Y K E L M G P W N K D E I S 92  
ACCACAGACGCGATCTTCGTCCAGCGGGATCTAAGCTGGTCCAGGGCTTCATGCCCCAC  
421 -----+-----+-----+-----+-----+-----+ 480  
TGGTGTCTGCGCTAGAAGCAGGTTCGCCCTAGACTTCGACCAGGTCCCGAAGTACGGGGTG

aa T T D A I F V Q R D L K L V Q G F M P H 112  
TTCTTCAGGCTGTTCCGGAGCACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCC  
481 -----+-----+-----+-----+-----+-----+ 540  
AAGAAGTCCGACAAGGCCTCGTGCCAGTTCGTTACCTGAAAAGTCTCCACCTCTCTCGG

aa F F R L F R S T V K Q V D F S E V E R A 132  
AGATTCATCATCAATGACTGGGTGAAGACACACAAAAGGTATGATCAGCAACTTGCTT  
541 -----+-----+-----+-----+-----+-----+ 600  
TCTAAGTAGTAGTTACTGACCCACTTCTGTGTGTGTTTTCCATACTAGTCGTTGAACGAA

aa R F I I N D W V K T H T K G M I S N L L 152

FIG. 1A

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GGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGGTGAATGCCCTCTACTTCAAC
601 -----+-----+-----+-----+-----+-----+ 660
CCCTTTCTCTCGGCACCTGGTTCGACTGTGCCGACCACGACCACTTACGGGAGATGAAGTTG
aa G K G A V D Q L T R L V L V N A L Y F N 172

GGCCAGTGGAAAGACTCCCTTCCCCGACTCCAGCACCCACCGCCGCTCTTCCACAAATCA
661 -----+-----+-----+-----+-----+-----+ 720
CCGGTCACCTTCTGAGGGAAGGGGCTGAGGTCGTGGGTGGCGGCGGAGAAGGTGTTTAGT
aa G Q W K T P F P D S S T H R R L F H K S 192

GACGGCAGCACTGTCTCTGTGCCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAG
721 -----+-----+-----+-----+-----+-----+ 780
CTGCCGTCGTGACAGAGACACGGGTACTACCGAGTCTGGTTGTTCAAGTTGATATGACTC
aa D G S T V S V P M M A Q T N K F N Y T E 212

TTCACCACGCCCGATGGCCATTACTACGACATCCTGGAAGTGCCTTACCACGGGGACACC
781 -----+-----+-----+-----+-----+-----+ 840
AAGTGGTGCGGGCTACCGGTAATGATGCTGTAGGACCTTGACGGGATGGTGGCCCTGTGG
aa F T T P D G H Y Y D I L E L P Y H G D T 232

CTCAGCATGTTTCATTGCTGCCCCCTTATGAAAAAGAGGTGCCTCTCTCTGCCCTCACCAAC
841 -----+-----+-----+-----+-----+-----+ 900
GAGTCGTACAAGTAACGACGGGGAATACTTTTTCTCCACGGAGAGAGACGGGAGTGGTTG
aa L S M F I A A P Y E K E V P L S A L T N 252

ATTCTGAGTGCCCGAGCTCATCAGCCACTGGAAGGCAACATGACCAGGCTGCCCCGCCTC
901 -----+-----+-----+-----+-----+-----+ 960
TAAGACTCACGGGTCGAGTAGTCGGTGACCTTTCCGTTGTACTGGTCCGACGGGGCGGAG
aa I L S A Q L I S H W K G N M T R L P R L 272

CTGGTTCTGCCCAAGTTCTCCCTGGAGACTGAAGTCGACCTCAGGAAGCCCCCTAGAGAAC
961 -----+-----+-----+-----+-----+-----+ 1020
GACCAAGACGGGTTCAAGAGGGACCTCTGACTTCAGCTGGAGTCCTTCGGGGATCTCTTG
aa L V L P K F S L E T E V D L R K P L E N 292

CTGGGAATGACCGACATGTTTCAGACAGTTTCAGGCTGACTTCACGAGTCTTTCAGACCAA
1021 -----+-----+-----+-----+-----+-----+ 1080
GACCCCTTACTGGCTGTACAAGTCGTCAAAGTCCGACTGAAGTGCTCAGAAAGTCTGGTT
aa L G M T D M F R Q F Q A D F T S L S D Q 312

GAGCCTCTCCACGTCGCGCAGGCGCTGCAGAAAGTGAAGATCGAGGTGAACGAGAGTGGC
1081 -----+-----+-----+-----+-----+-----+ 1140
CTCGGAGAGGTGCAGGCGGTCCGCGACGCTTTCACTTCTAGCTCCACTTGCTCTCACCG
aa E P L E V A Q A L Q K V K I E V N E S G 332

ACGGTGGCCTCCTCATCCACAGCTGTCTAGTCTCAGCCCGCATGGCCCCCGAGGAGATC
1141 -----+-----+-----+-----+-----+-----+ 1200
TGCCACCGGAGGAGTAGGTGTGACAGTATCAGAGTCGGGCGTACCGGGGGCTCCTCTAG
aa T V A S S S T A V I V S A R M A P E E I 352

ATCATGGACAGACCCCTTCCTCTTTGTGGTCCGGCACAACCCACAGGAACAGTCCCTTTTC
1201 -----+-----+-----+-----+-----+-----+ 1260
TAGTACCTGTCTGGGAAGGAGAAACACCAAGCCGCTGTTGGGGTGTCTTGTTCAGGAAAAG
aa I M D R P F L F V V R H N P T G T V L F 372

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FIG. 1B

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ATGGGCCAAGTGATGGAACCCCTGACCCTGGGGAAAGACGCCTTCATCTGGGACAAACTG  
1261 -----+-----+-----+-----+-----+-----+ 1320  
TACCCGGTTCACTACCTTGGGACTGGGACCCCTTTCTGCGGAAGTAGACCCTGTTTTGAC  
M G Q V M E P \* 379  
GAGATGCATCGGGAAAGAAGAACTCCGAAGAAAAGAATTTTAGTGTTAATGACTCTTTC  
1321 -----+-----+-----+-----+-----+-----+ 1380  
CTCTACGTAGCCCTTTCTTCTTTGAGGCTTCTTTTCTTAAATCACAACTACTGAGAAAG  
TGAGGAAGAGAAGACATTTGCCTTTTGTAAAAGATGGTAAACCAGATCTGTCTCCAAG  
1381 -----+-----+-----+-----+-----+-----+ 1440  
ACTTCCTTCTCTCTGTAAACGGAAACAATTTTCTACCATTGGTCTAGACAGAGGTTTC  
ACCTTGGCCTCTCCTTGGAGGACCTTTAGGTCAAACCTCCCTAGTCTCCACCTGAGACCCT  
1441 -----+-----+-----+-----+-----+-----+ 1500  
TGGAAACCGGAGAGGAACCTCCTGGAATCCAGTTTGAGGGATCAGAGGTGGACTCTGGGA  
GGGAGAGAAGTTTGAAGCACAACTCCCTTAAGGTCTCCAAACCAGACGGTGACGCCTGCG  
1501 -----+-----+-----+-----+-----+-----+ 1560  
CCCTCTCTTCAAACCTCGTGTGAGGGAATTCAGAGGTTGGTCTGCCACTGCGGACGC  
GGACCATCTGGGGCACCTGCTTCCACCCGTCTCTCTGCCACTCGGGTCTGCAGACCTGG  
1561 -----+-----+-----+-----+-----+-----+ 1620  
CCTGGTAGACCCCGTGGACGAAGGTGGGCAGAGAGACGGGTGAGCCAGACGTCTGGACC  
TTCCCACTGAGGCCCTTTGCAGGATGGAACCTACGGGGCTTACAGGAGCTTTTGTGTGCCT  
1621 -----+-----+-----+-----+-----+-----+ 1680  
AAGGGTGACTCCGGGAACGTCTTACCTTGATGCCCGAATGTCTCGAAAACACACGGA  
GGTAGAAACTATTTCTGTTCAGTCACATTGCCATCACTCTTGTACTGCCTGCCACCGCG  
1681 -----+-----+-----+-----+-----+-----+ 1740  
CCATCTTTGATAAAGACAAGGTCAGTGTAAACGGTAGTGAGAACATGACGGACGGTGGCGC  
GAGGAGGCTGGTGACAGGCCAAAGGCCAGTGGAAGAAACACCCCTTCATCTCAGAGTCCA  
1741 -----+-----+-----+-----+-----+-----+ 1800  
CTCCTCCGACCACTGTCCGGTTTCCGGTCTCTTCTTTGTGGAAAGTAGAGTCTCAGGT  
CTGTGGCACTGGCCACCCCTCCCCAGTACAGGGGTGCTGCAGGTGGCAGAGTGAATGTCC  
1801 -----+-----+-----+-----+-----+-----+ 1860  
GACACCGTGACCGGTGGGGAGGGGTCTGTCTCCACGACGTCCACCGTCTCACTTACAGG  
CCCATCATGTGGCCCAACTCTCCTGGCCTGGCCATCTCCCTCCCCAGAAACAGTGTGCAT  
1861 -----+-----+-----+-----+-----+-----+ 1920  
GGGTAGTACACCGGTTGAGAGGACCGGACCGGTAGAGGGAGGGTCTTTGTACACGTA  
GGGTATTTTGGAGTGTAGGTGACTTGTCTTACTCATGAAGCAGATTTCTGCTTCCTTTT  
1921 -----+-----+-----+-----+-----+-----+ 1980  
CCCAATAAAACCTCACATCCACTGAACAAATGAGTAACCTTCGTCTAAGACGAAGGAAAA  
ATTTTTATAGGAATAGAGGAAGAAATGTCAGATGCGTGCCAGCTCTTCACCCCCAATC  
1981 -----+-----+-----+-----+-----+-----+ 2040  
TAAAAATATCCTTATCTCTTCTTACAGTCTACGCACGGGTGAGAAAGTGGGGGGTTAG

FIG. 1C

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2041 TCTTGGTGGGGAGGGGTGTACCTAAATATTATCATATCCTTGCCCTGAGTGCTTGTTA  
-----+-----+-----+-----+-----+ 2100  
AGAACCACCCCTCCCCACATGGATTTATAAATAGTATAGGAACGGGAACCTCACGAACAAT  
  
2101 GAGAGAAAGAGAACTACTAAGGAAAATAATATTATTAAACTCGCTCCTAGTGTTTCTTT  
-----+-----+-----+-----+-----+ 2160  
CTCTCTTTCTCTTGATGATTCCTTTTATTATAATAAATTGAGCGAGGATCACAAAGAAA  
  
2161 GTGGTCTGTGTACCGTATCTCAGGAAGTCCAGCCACTTGACTGGCACACACCCCTCCGG  
-----+-----+-----+-----+-----+ 2220  
CACCAGACACAGTGGCATAGAGTCCTTCAGGTCGGTGAACCTGACCGTGTGTGGGGAGGCC  
  
2221 ACATCCAGCGTGACGGAGCCCACTGCGCACCTTGTGGCCGCTGAGACCTCGCGCCCC  
-----+-----+-----+-----+-----+ 2280  
TGTAGGTCGCACCTCGCTCGGGGTGTACGGTGGAAACACCGCGGACTCTGGGAGCGCGGGG  
  
2281 CCGCGCCCCCGCGCCCTCTTTTCCCTTGATGGAAATTGACCATACAATTCATCCT  
-----+-----+-----+-----+-----+ 2340  
GGCGCGGGGGCGCGGGGAGAAAAGGGGAACCTCTTAACCTGGTATGTTAAAGTAGGA  
  
2341 CCTTCAGGGGATCAAAGGACGGAGTGGGGGGACAGAGACTCAGATGAGGACAGAGTGGT  
-----+-----+-----+-----+-----+ 2400  
GGAAGTCCCCTAGTTTTCCTGCCTCACCCCCCTGTCTGTAGTCTACTCCTGTCTCACA  
  
2401 TTCCAATGTGTTCAATAGATTTAGGAGCAGAAATGCAAGGGGCTGCATGACCTACCAGGA  
-----+-----+-----+-----+-----+ 2460  
AAGGTTACACAAGTTATCTAAATCCTCGTCTTTACGTTCCCGACGTACTGGATGGTCCT  
  
2461 CAGAACTTTCCCAATTACAGGGTGACTCACAGCCGCATTGGTGACTCACTTCAATGTGT  
-----+-----+-----+-----+-----+ 2520  
GTCTTGAAAGGGGTTAATGTCCCACTGAGTGTGCGCGTAACCACTGAGTGAAGTTACACA  
  
2521 CATTTCCGGCTGCTGTGTGTGAGCAGTGGACACGTGAGGGGGGGTGGGTGAGAGAGACA  
-----+-----+-----+-----+-----+ 2580  
GTAAAGGCCGACGACACACTCGTCACCTGTGCACTCCCCCCCCACCACTCTCTCTGT  
  
2581 GGCAGCTCGGATTCAACTACCTTAGATAATATTCTGAAAACCTACCAGCCAGAGGGTAG  
-----+-----+-----+-----+-----+ 2640  
CCGTCGAGCCTAAGTTGATGGAATCTATTATAAAGACTTTTGGATGGTCGGTCTCCCATC  
  
2641 GGCACAAAGATGGATGTAATGCACCTTGGGAGGCCAAGGCGGGAGGATTGCTTGAGCCCA  
-----+-----+-----+-----+-----+ 2700  
CCGTGTTTCTACCTACATTACGTGAAACCTCCGGTTCGCCCCCTCCTAACGAACCTCGGGT  
  
2701 GGAGTTCAAGACCAGCCTGGGCAACATACCAAGACCCCGTCTCTTAAAAATATATATA  
-----+-----+-----+-----+-----+ 2760  
CCTCAAGTTCTGGTCGGACCCGTTGTATGGTTCTGGGGGAGAGAAATTTTATATATAT  
  
2761 TTTTAAATATACTTAAATATATATTTCTAATATCTTTAAATATATATATATTTTAAAG  
-----+-----+-----+-----+-----+ 2820  
AAAATTTATATGAATTTATATATAAAGATTATAGAAATTTATATATATATATAAAATTC  
  
2821 ACCAATTTATGGGAGAATTGCACACAGATGTGAAATGAATGTAATCTAATAGAAGC  
-----+-----+-----+-----+-----+ 2876  
TGGTAAATACCCTCTTAACGTGTGTCTACACTTTACTTACATTAGATTATCTTCG

FIG. 1D

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MQMSPALTCLVLGLALVFGECSA  
Signal peptide

VHHPPSYVAHLASDFGVRVFQOVAQASKDRNVVFSPIGVASVLAMLQLTTGGETQQQIQ  
AMGFKIDDKGMAPALRHLYKELMGFWNKDEISTTDAIFVQDLKLVQGFMPHFFRLFRST  
VKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP  
DSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDLSMFIAAP  
YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFR  
QFQADFTSLSDQEPLHVAQALQVKIEVNESGTVASSSTAVIVSARMAPEEIIMDRPFLF  
VVRHNPTGTVLFMGQVMEP

FIG. 2A

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10 20 30 40 50 60  
VHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPIGVASVLAMLQTTGGETQQQIQ

70 80 90 100 110 120  
AMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQORDLKLVOGFMPHFFRLFRST

130 140 150 160 170 180  
VKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP

190 200 210 220 230 240  
DSSTHRRFLFKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLMSFIAAP

250 260 270 280 290 300  
YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFR

310 320 330 340 350 360  
QFQADFTSLSDQEPLHVAQALQVKIEVNESGTVASSSTAVIVSARMAPEEIIIMDRPFLF

370  
VVRHNPTGTVLFMGQVMEP

FIG. 2B

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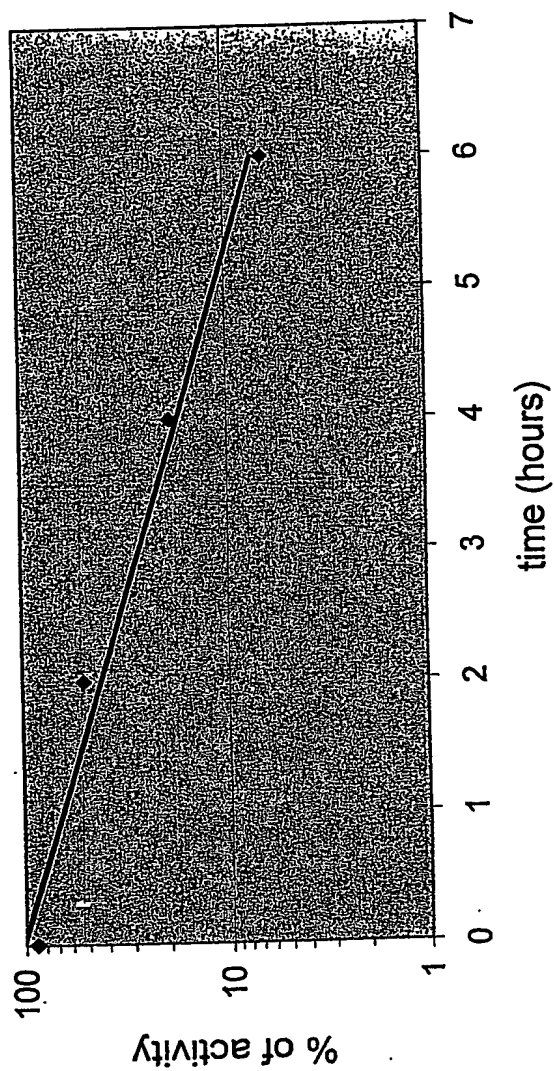


FIG. 3

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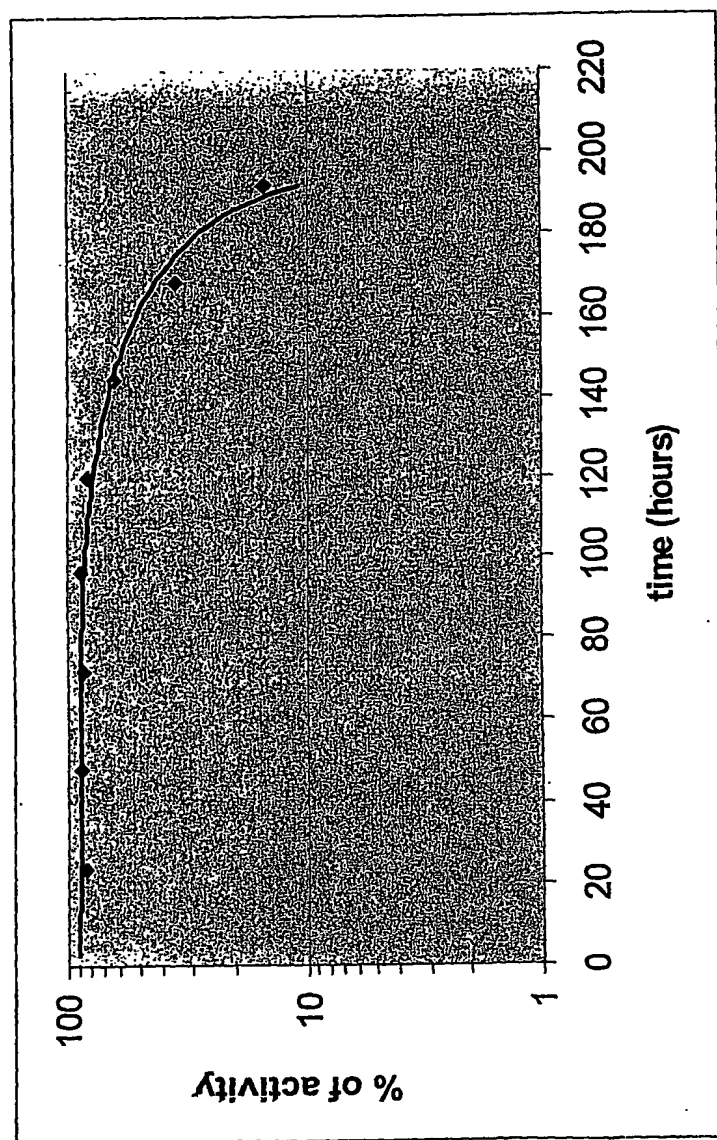


FIG. 4



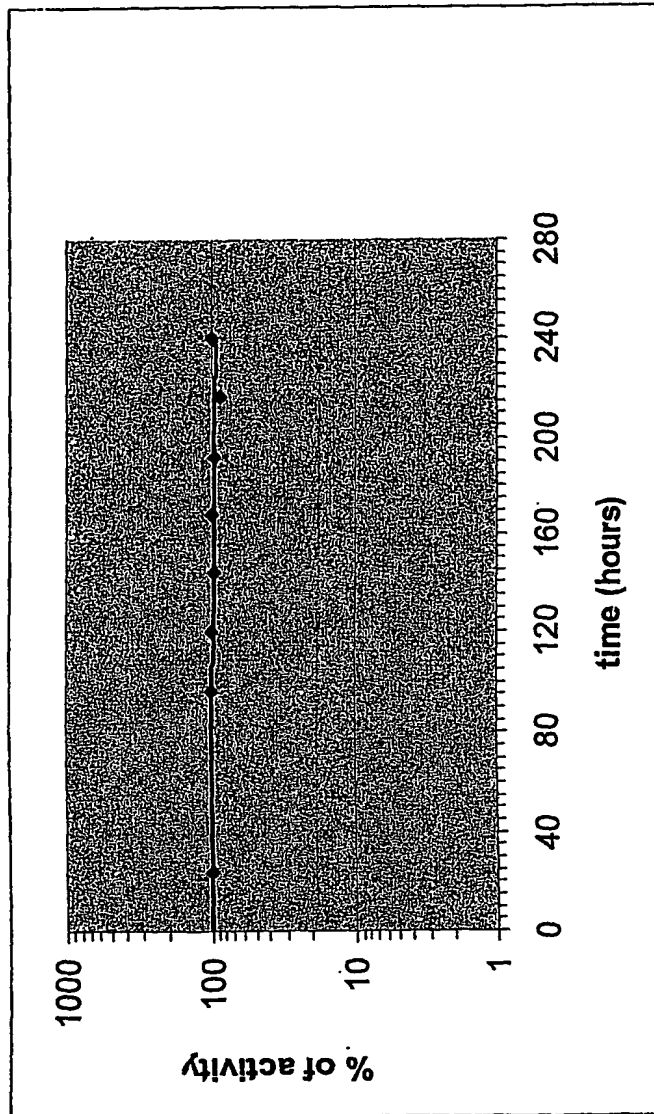


FIG. 5

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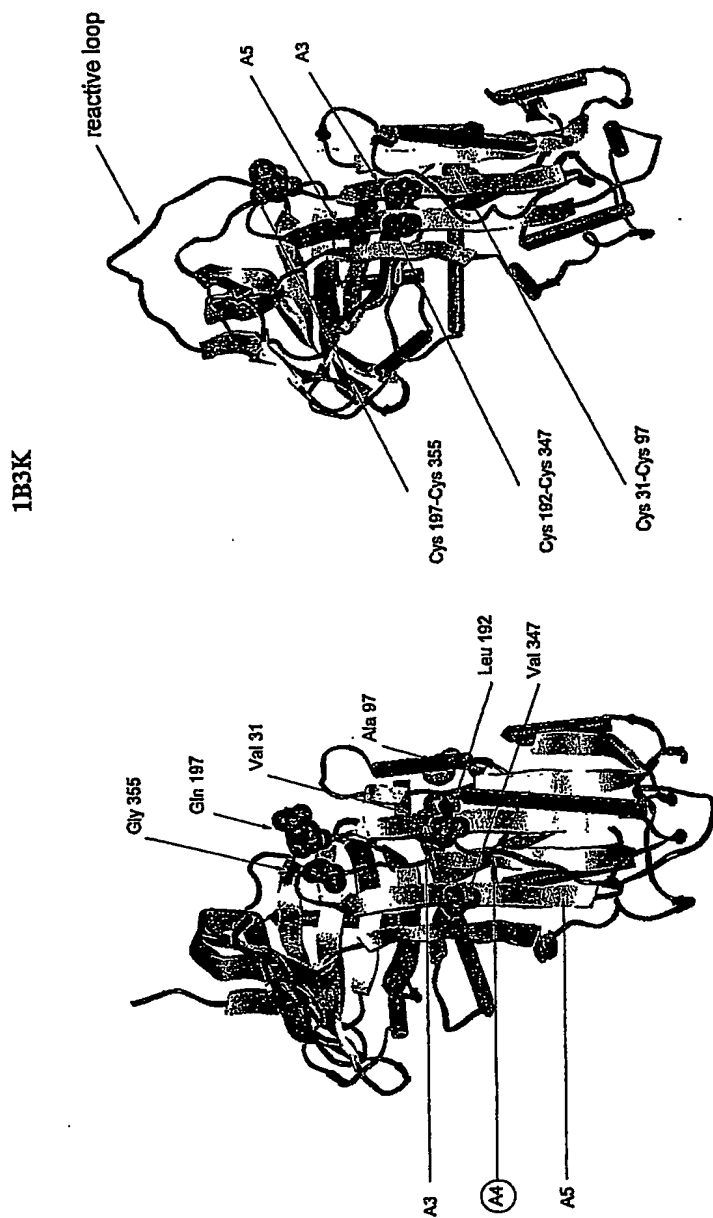


FIG. 6

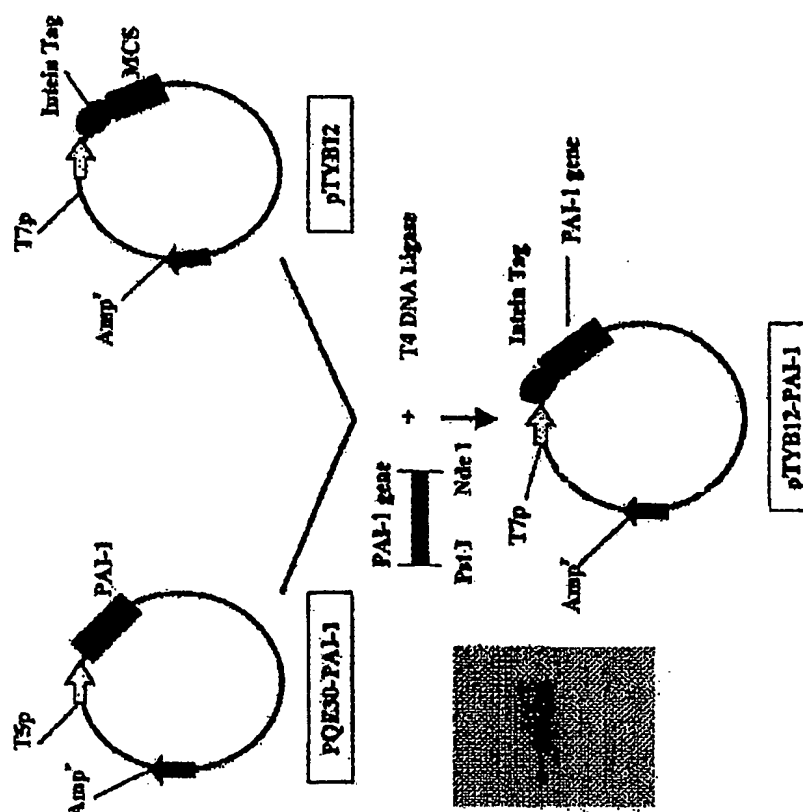


FIG. 7

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FIG. 8B



FIG. 8A

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FIG. 9B

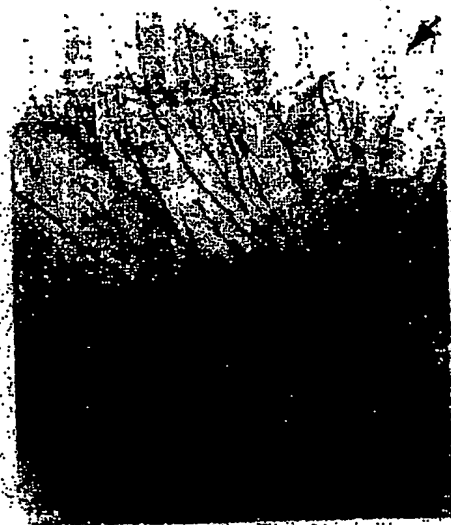


FIG. 9A

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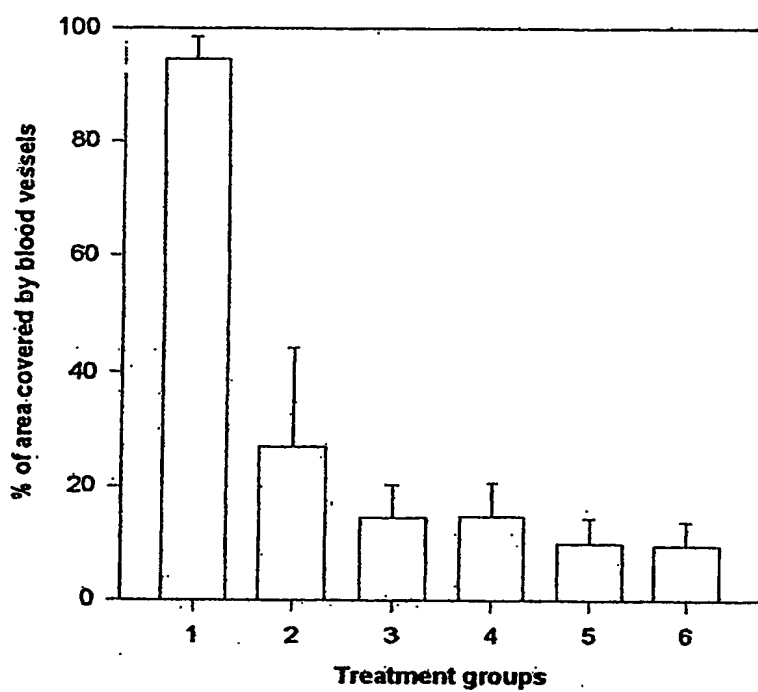


FIG. 10

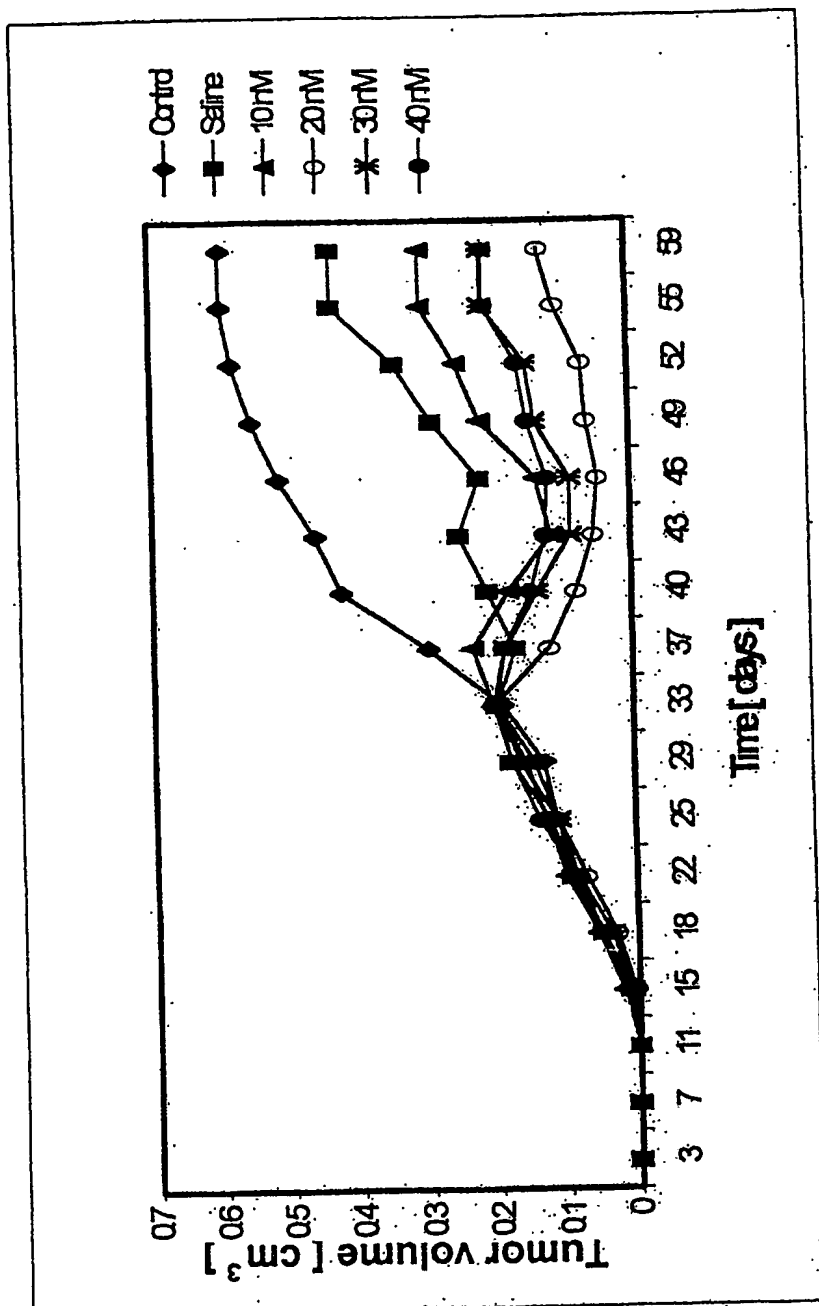


FIG. 11

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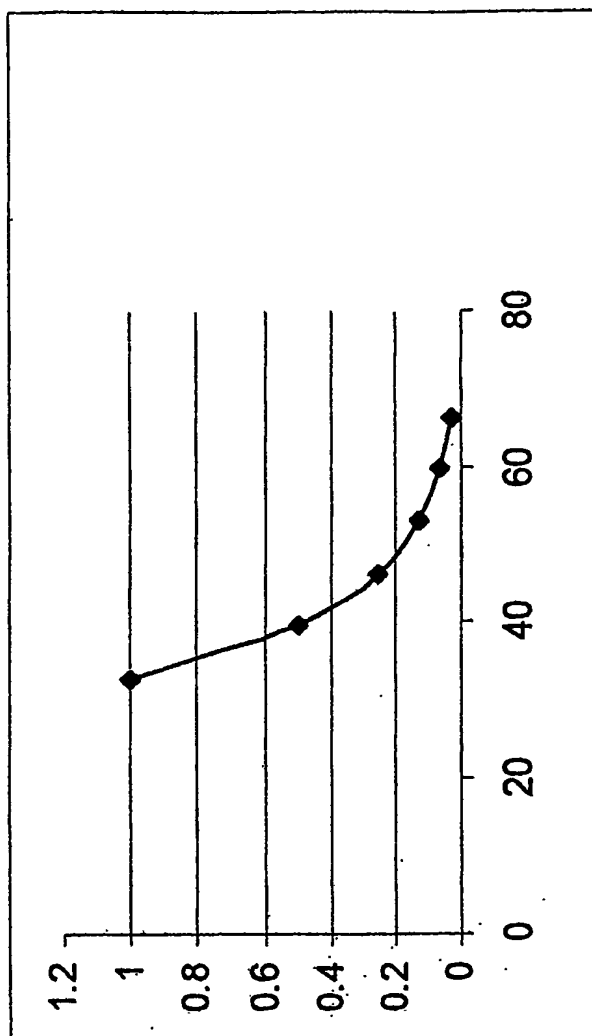


FIG. 12



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